

Claim 24 (Withdrawn): The pair of polymerase chain reaction primers of claim 23, wherein said prokaryote is selected from the group consisting of *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Helicobacter pylori*, *Methanococcus jannaschii*, *Archaeoglobus fulgidus* and *Synechocystis* sp. PCC6803.

Claim 25 (Currently amended): An allele specific oligonucleotide comprising a sequence of nucleotides adapted for effectively hybridizing only with at least one specific simple sequence repeat of a polymorphic mono- or dinucleotide simple sequence repeat locus in a genome of *Listeria monocytogenes* ~~prokaryote~~, under stringent allele specific oligonucleotide hybridization conditions of (i) a hybridization solution of 2 x standard sodium citrate (SSC) and 0.1 % sodium dodecyl sulfate (SDS); (ii) a hybridization temperature of from 42 °C to  $T_m - 5$  °C for 30 minutes to overnight, wherein  $T_m$  is estimated as  $2 \times (\text{the number of A plus T residues}) + 4 \times (\text{the number of G plus C residues})$ ; and (iii) post hybridization washes with 0.75 x SSC and 0.1 % SDS at a temperature from 42 °C to  $T_m - 5$  °C, wherein said polymorphic simple sequence repeat locus comprises at least four nucleotides in at least one of its polymorphs, and whereas said polymorphic simple sequence is in a non-coding region of said *Listeria monocytogenes* genome.

Claim 26 (Original): The allele specific oligonucleotide of claim 25, wherein said sequence of nucleotides is perfectly complementary to said specific simple sequence repeat.

Claim 27 (Original): A hybrid of the allele specific oligonucleotide of claim 25 and said specific simple sequence repeat.

Claim 28 (Withdrawn):. The allele specific oligonucleotide of claim 25, wherein said polymorphic simple sequence locus is in a non-coding region of said genome.

Claim 29 (Withdrawn): The allele specific oligonucleotide of claim 25, wherein said prokaryote is of the genus *Escherichia*.

Claim 30 (Withdrawn): The allele specific oligonucleotide of claim 29, wherein said prokaryote is *Escherichia coli*.

Claim 31 (Cancelled)

Claim 32 (Cancelled)

Claim 33 (Withdrawn): The allele specific oligonucleotide of claim 25, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilus*, *Mycoplasma*, *Helicobacter*, *Methanococcus*, *Archaeoglobus* and *Synechocystis*.

Claim 34 (Withdrawn): The allele specific oligonucleotide of claim 33, wherein said prokaryote is selected from the group consisting of *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Helicobacter pylori*, *Methanococcus jannaschii*, *Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.

Claim 35 (Currently amended): A primer having a sequence adapted for amplification of a polymorphic mono- or dinucleotide simple sequence repeat locus in a genome of *Listeria monocytogenes* prokaryote, said polymorphic simple sequence repeat locus comprising at least four nucleotides in at least one of its polymorphs, wherein said polymorphic simple sequence is in a non-coding region of said *Listeria monocytogenes* genome.

Claim 36 (Cancelled)

Claim 37 (Withdrawn): The primer of claim 35, wherein said

prokaryote is of the genus *Escherichia*.

Claim 38 (Withdrawn): The primer of claim 37, wherein said prokaryote is *Escherichia coli*.

Claim 39 (Cancelled)

Claim 40 (Cancelled)

Claim 41 (Withdrawn): The primer of claim 35, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilus*, *Mycoplasma*, *Helicobacter*, *Methanococcus*, *Archaeoglobus* and *Synechocystis*.

Claim 42 (Withdrawn): The primer of claim 41, wherein said prokaryote is selected from the group consisting of *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Helicobacter pylori*, *Methanococcus jannaschii*, *Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.

Claim 43 (Currently amended): A DNA chip comprising a surface and a plurality of allele specific oligonucleotides attached thereto, each of said plurality of allele specific oligonucleotides including a sequence of nucleotides adapted for effectively hybridizing only with a specific simple sequence repeat of a polymorphic mono- or dinucleotide simple sequence repeat locus in a genome of *Listeria monocytogenes*—a prokaryote, under stringent allele specific oligonucleotide hybridization conditions of (i) a hybridization solution of 2 x standard sodium citrate (SSC) and 0.1 % sodium dodecyl sulfate (SDS); (ii) a hybridization temperature of from 42 °C to  $T_m - 5$  °C for 30 minutes to overnight, wherein  $T_m$  is estimated as  $2 \times (\text{the number of A plus T residues}) + 4 \times (\text{the number of G plus C residues})$ ; and (iii) post hybridization washes with 0.75 x SSC and 0.1 % SDS at a temperature from 42 °C to  $T_m - 5$  °C, wherein said polymorphic simple sequence repeat locus comprises at least four nucleotides in at least one of its polymorphs, and whereas said polymorphic simple sequence is

in a non-coding region of said *Listeria monocytogenes* genome.:-

Claim 44 (Original): The DNA chip of claim 43, wherein said sequence of nucleotides is perfectly complementary to said specific simple sequence repeat.

Claim 45 (Cancelled)

Claim 46 (Withdrawn): The DNA chip of claim 43, wherein said prokaryote is of the genus *Escherichia*.

Claim 47 (Withdrawn): The DNA chip of claim 46, wherein said prokaryote is *Escherichia coli*.

Claim 48 (Cancelled)

Claim 49 (Cancelled)

Claim 50 (Withdrawn): The DNA chip of claim 43, wherein said prokaryote is of a genus selected from the group consisting of *Haemophilus*, *Mycoplasma*, *Helicobacter*, *Methanococcus*, *Archaeoglobus* and *Synechocystis*.

Claim 51 (Withdrawn): The DNA chip of claim 50, wherein said prokaryote is selected from the group consisting of *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Helicobacter pylori*, *Methanococcus jannaschii*, *Archaeoglobus fulgidus* and *Synechocystis sp. PCC6803*.